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OM protein - nucleic search, using frame_Plus_P2n model

Run on: April 5, 2003, 01:50:12 ; Search time 287 Seconds
 (without alignments)
 3452.541 Million cell updates/sec

Title: US-09-847-081B-2
 Perfect score: 2270
 Sequence: 1 MSMVALLWVSPTEVSNG.....IAYAKSLVPPNRTSSPLAKT 440

Scoring table: Blosum62

Xgapext 10.0 Xgapext 0.5
 Ygapext 10.0 Ygapext 0.5
 Fgapext 6.0 Fgapext 7.0
 Dgap 6.0 Delett 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

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-MODEL:frame+P2n.model -DEV=xmlP
-Q=Cgn2_1/USP0_5pool/US09847081/runat_01042003_120128_26729/app_query.fasta_1..583
-DB=N_Geneset_10102 -QBWT=fastap -SUFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -STAR=1 -END=1 -MATRIX=blossom62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFILE=pto -NORM=EXT -HEAPSIZE=500 -MINLEN=2000000000
-USER=US09847081_@runat_01042003_120128_26729 -NCPU=6 -ICPU=3
-NO_XLPPX -NO_NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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3: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1982.DAT;*
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6: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1985.DAT;*
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23: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2001B.DAT;*
24: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2002.DAT;*
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Database :

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RESULT 1
ID AA166366 standard; cDNA; 1728 BP.
XX
AC AA166366;
XX
DT 29-JAN-2002 (first entry)
XX
DE Nicotiana tabacum phytene synthase coding sequence #1.
XX
XX
KW Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant;
KW plant growth regulator; herbicidal; tobacco; ss.
XX
OS Nicotiana tabacum.
XX
```

SUMMARIES

	Result No.	Score	Query	Match	Length	DB ID	Description
	1	2210	100.0	1728	24	AA166366	Nicotiana tabacum phytene synthase
	2	1826	80.4	1826	19	AAV03880	Nicotiana tabacum phytene synthase
	3	1801	79.3	1712	24	AA166367	Phytene synthase
	4	1739	79.3	1814	19	AAV03881	Phytene synthase
	5	1774	78.1	1795	19	AAV03878	Phytene synthase
	6	1762	77.6	1316	19	AAV03879	Malon phytoene synthase
	7	1755	77.1	1591	17	AAQ9323	MTOH5, modified ph
	8	1744	76.8	1239	19	AAV1247	cDNA encoding a ph
	9	1737	76.5	1239	21	AAZ91482	Tomat fruit ripen
	10	1729	76.2	1646	12	AAQ12495	Nucleic acid encod
	11	1595	70.3	2868	19	AAV16951	Nucleic acid encod
	12	1557	68.6	1921	19	AAV16949	Nucleic acid encod
	13	1542	67.9	1566	21	AAU8162	Arabidopsis thalia
	14	1542	67.9	1703	21	AAC5120	Nucleic acid encod
	15	1531	67.4	2085	19	AAV16948	Nucleic acid encod
	16	1523	67.1	1932	19	AAV16950	Corn phytoene s
	17	1514	66.7	2585	23	ABA1600	Rice phytoene synt
	18	1431.5	63.1	1304	24	ABA97361	Nucleotide sequenc
	19	1293	61.4	1397	21	AAZ29145	Soybean phytoene s
	20	1252.5	55.2	1448	21	AAZ29139	Corn phytoene synt
	21	1078	52.1	1021	21	AAZ29146	Wheat phytoene syn
	22	1033.5	45.5	3485	13	AAQ9121	Fragment of Gm05
	23	1033	45.5	992	21	AAZ29144	Soybean phytoene s
	24	992	43.7	1060	21	AAZ29143	Rice phytoene synt
	25	781.5	34.4	888	21	AAZ29140	Corn phytoene synt
	26	511	22.5	476	21	AAZ29142	Rice phytoene synt
	27	468	20.6	684	22	AAH44248	Phycomitrella pat
	28	458.5	20.2	1500	15	AAQ64910	Thermophil
	29	444.2	19.5	749	19	AAV03882	Phytene synthase
	30	420	18.5	766	17	AAZ29141	Rice phytoene synt
	31	378	16.7	56609	21	AAA81459	N. meningitidis pa
	32	378	16.7	349980	21	AAF21609	Neisseria meningit
	33	378	16.7	1437668	21	AAA81490	N. meningitidis B
	34	364	16.0	1198	12	AAQ13718	Phytene synthase
	35	364	16.0	1198	17	AAU10791	Phytene synthase
	36	364	16.0	1198	17	AAU1743	Phytene synthase
	37	364	16.0	1198	17	AAU1093	E. herbicola Phyto
	38	364	16.0	1198	18	AAU1543	Erwinia herbicola
	39	363.5	16.0	930	18	AAU6534	Nucleotide sequenc
	40	350.5	15.4	1232	19	AAV19122	SSU/CrtB (phytene
	41	350.5	15.4	1232	20	AAU2063	Nucleotide sequenc
	42	350.5	15.4	1232	24	ABA97354	Sequence encoding
	43	349.5	15.4	6918	11	AAU02299	Fragment contig, PT
	44	347.5	15.3	1386	13	AAQ29122	E. ureodovora Phyto
	45	344.5	15.2	930	18	AAX23885	Erwinia herbicola

ALIGNMENTS

	RESULT 1	ID	AAI66366 standard; cDNA; 1728 BP.
XX			
AC	AAI66366;		
XX			
DT	29-JAN-2002 (first entry)		
XX			
DE	Nicotiana tabacum phytene synthase coding sequence #1.		
XX			
KW	Phytene synthase; zeta carotene desaturase; herbicide; transgenic plant;		
KW	plant growth regulator; herbicidal; tobacco; ss.		
XX			
OS	Nicotiana tabacum.		
XX			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Key	Location/Qualifiers
FT	24..1566
FT	/*tag- a

FT	/product- "phytoene synthase"		
XX			
PN	DE10022362-A1.		
XX			
PD	15-NOV-2001.		
XX			
PF	08-MAY-2000; 2000DE-1022362.		
XX			
PR	08-MAY-2000; 2000DE-1022362.		
XX			
PA	(FARB) BAYER AG.		
XX			
PI	Busch M., Hain R;		
XX			
WPI:	2002-027336/04.		
DR	P-FSDB; AAM51841.		
XX			
PT	New nucleic acid encoding tobacco zeta-carotene desaturase, useful for screening compounds with herbicidal activity		
XX			
PS	Claim 14: Page 12-17; 44pp; German.		
XX			
CC	The present invention provides the protein and coding sequences of phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum. The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.		
CC			
CC			
CC			
SQ	Sequence 1728 BP; 513 A; 290 C; 433 G; 492 T; 0 other;		
XX			
Alignment Scores:			
Pred. No. :	7.89e-234	Length:	1728
Score:	2270.00	Matches:	440
Percent. Similarity:	100.0%	Conservative:	0
Best. Local. Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	24	Gaps:	0
US-09-847-081B-2 (1-440) x AAI66366 (1-1728)			
Qy	1. MetSerMetSerValAlaLeuLeuProThrSerProThrSerValSerAsnGly 20		
Db	244 ATAGCATGTCTGTGCttGtttGtttGtttGtttGtttGtttGG 303		
Qy	21 ThrglyleuLeuAspSerValArgGluGlyAsnArgValPheValSerArgPheLeu 40		
Db	304 ACAGGATGTTGGATTCACTGCCACUTCCAGGAAACCGCCTCATCCAGGTCCTA 363		
Qy	41 AlAArgAspArgAsnLeuMetPtpAsnGlyArgLileLysLysGlyGlyArgGlnArgTrp 60		
Db	364 GCCTCGAGATAAGGAAATTGTTGTTGGAATTGGGAAATCAAGAAAGCTGG 423		
Qy	61 AsnPhgGlySerLeuIleAlaAspProArgTyrsercyLeuGlySerArgThrGlu 80		
Db	424 AATTGTTGGCTTAACTGCTGATCCAGAATTCATGCTGGTGGATCAAAGTAA 483		
Qy	81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100		
Db	484 AACGGAAACACTTCTCIGTACAGTCCAGTTGGTGCCTAGCCAGCTGAGAAATGACT 543		
Qy	101 ValSerSerGluLysLysValtyrAspValValLeuLysGlnAlaAlaLeuValLysArg 120		
Db	544 GTGTCATGAGAAAAGCTGATGAGTGTTTAAAGCAGGCCAGTTAGTGAGAGG 603		
Qy	121 GluLeuIrgSerThrAspAspLeuGlyLysProAspIleValValProGlyAsnLeu 140		
Db	604 CAGCTGAGATCTACCGATGATTAGATGTTAGCTGAGCCGATATGTTGTCAGGGATTG 663		
Qy	141 GlyLeuLeuSerGluAlaIatyrAspArgCysGlyGluValCysAlaGluIutyrAlaLystr 160		
Db	664 GGCTTGTTGAGTGAAGCATATGATGCTGTTGCGCAAGTAGTGCAGATGAAAGACA 723		
		RESULT 2	
		AAV03880	
ID	AAV03880 standard; cDNA; 1826 BP.		
XX			
DE			
XX			
AC			
XX			
DT	29-APR-1998 (first entry)		
XX			
Phytoene synthase coding sequence from N. tabacum.			
XX			
KW			
XX			
ultra violet absorber; food colour; ss.			
XX			
Nicotiana tabacum.			
XX			
FH			
Key			
		Location/Qualifiers	

KW Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant;
 KW Plant growth regulator; herbicidal; tobacco;
 XX Nicotiana tabacum.

XX Location/Qualifiers
 333..1565
 /*tag- a
 FT /product= "phytoene synthase"

PH DE10022362-A1.
 PN 08-MAY-2000; 2000DE-1022362.
 XX 15-NOV-2001.
 PD 08-MAY-2000; 2000DE-1022362.
 PR 08-MAY-2000; 2000DE-1022362.
 XX (FARS) BAYER AG.
 PA Busch M, Hain R;
 XX WPI; 2002-027336/04.
 DR P-PSDB; AAM51842.
 XX New nucleic acid encoding tobacco zeta-carotene desaturase, useful for screening compounds with herbicidal activity

PT PT screening compounds with herbicidal activity

XX Claim 14: Page 21-26; 44PP; German.

XX The present invention provides the protein and coding sequences of phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum. The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.

XX Sequence 1712 BP; 540 A; 265 C; 421 G; 475 T; 11 other;

Alignment Scores:

Pred. No :	2.0e-183	Length:	1712	QY 3 MetSerValAlaLeuLeuIrrpValIserProThrSerGluValIserAsnGlyThrGly 22
Score:	1801.00	Matches:	357	Db 333 ATGCTGTGGCTTGTATGGTTCTACCT--TGTGAAGTCAAATGGACAGGA 389
Percent Similarity:	87.93%	Conservative:	29	QY 23 LeuLeuAspSerValArgLleuGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
Best Local Similarity:	81.12%	Mismatches:	24	Db 390 TCTGGATTCAGTCGGAGGAAACGGTTTTGATCTCG-----AG 437
Query Match:	79.34%	Indels:	29	QY 43 AspArgAsnLeuMetTrpAsnGlyArgLleuLysGlyGlyArgLleuTrpAsnPhe 62
DB:	24	Gaps:	4	Db 438 CATGGAAATTACTGTGCAATGAGAGAACACAGAGGTGIGAAACAAAGGTGAATT 497
				QY 63 GlySerLeuIleAlaAspProArgTyrosCysLeuGlyIserArgThrGlyLysGly 82
				Db 498 GGT-----500
				QY 83 SerThrPheSerValGlnSerSerLeuAlaSerProAlaGlyGluMet---ThrVal 101
				Db 501 -----TCCTTAAGTCCTGATGCTGGATGGCTACACGGCGGAAATGGCACCATG 551
				QY 102 SerSerGluLysLysValTyrraspValValLeuLysGlnAlaAlaLeuValLysArgGln 121
				Db 552 ACATCAGAACAGATGGTTATGATGEGTTAACACGCAGCTTGTGACCTCTAG 611
				RESULT 4 AAV03881 ID : AAV03881 standard; cDNA: 1814 BP. XX AC XX DT 29-APR-1998 (first entry)

Phytoene synthase coding sequence from N. tabacum.
 XX Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;
 KW ultra violet absorber; food colour; ss.
 XX Nicotiana tabacum.

Location/Qualifiers
 FH CDS 363..195 /*tag= a.
 US5705624-A.
 XX PD 06-JAN-1998.

XX 27-DEC-1995; 95US-0579667.
 XX 27-DEC-1995; 95US-0579667.

XX (DELL/) DELLA-CIOPPA, G. R.
 (FIZZ/) FITZMAURICE W. P.
 (GRILL/) GRILL, L. K.
 (HELL/) HELLMANN, G. M.
 (KUMA/) KUMAGAI, M. H.
 PI Della-Cioppa, GR., Fitzmaurice, WP., Grill, L.K., Hellmann, GM.;
 PI Kumagai, MH;

XX WPI: 1998-086196/08.
 DR P-PSDB; AAW41060.
 XX PT DNA encoding tobacco phytoene synthase polypeptides - useful for
 PT producing recombinant polypeptides or transgenic plants
 XX Claim 1; Column 33-36; 25pp; English.
 CC This sequence encodes the phytoene synthetase from Nicotiana tabacum.
 CC The phytoene synthetase coding sequence represents a cDNA of the
 CC invention. The isolated nucleic acid molecules are used for producing to
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.

XX Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.65e-183 Length: 1814
 Score: 179.00 Matches: 356
 Percent Similarity: 87.93% Conservative: 30
 Best Local Similarity: 81.9% Mismatches: 24
 Query Match: 79.25% Indels: 29
 DB: 19 Gaps: 4

US-09-847-081B-2 (1-440) x AAV03881 (1-1814)

Qy 3 MetSerValAlaLeuLeuPheValaSerProThrSerGluValSerAsnGlyLysGly 22
 DB 363 ATGGCTGTGCCCTGTATGGGTGTTACCT--TGTGAAGTCAAATGGACAGA 419
 Qy 23 LeuLeuAlaPheSerValArgLysGlyLysGlyArgLysValSerArgPheLeuAlaArg 42
 DB 420 TTCTGGGATCCTCCGGGAAACCGGTTTTTCCTCGC---AGG 467
 Qy 43 AspArgAlaLeuMetTrpAsnGlyArgLysGlyArgLysGlyArgLysGly 62
 DB 468 CATGGATTATGTGGATGAGAACAGAGGGAAATT 527
 Qy 63 GlySerLeuLeuAlaAspProArgTy-SerCysLeuGlyGlySerArgThrGluLysGly 82
 DB 528 GGT----- 530
 Qy 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaSerAlaSerProAlaSerAlaSerAlaSerAlaSerAlaSerArgTriPpO 381
 Qy 342 ArgValLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspLysIlePhe 341
 DB 1242 AGGTCTACTTACCTCAGATGATTACACGAGGTCTCTGCAGCATGAGATATT 1301
 Qy 342 AlaGlyArgValIhrAspLysTrpArgAsnPhemethylsLysGlnIleGlnArgAlaArg 361
 DB 1302 GCTGAAAGTGACTGATGATAAGTGAGAAGCAATCCAGGGCAAGA 1331
 Qy 362 LysPhePheAspGluUserGluLysGlyValThrGluLeuAspSerAlaSerArgTriPpO 381
 DB 1362 AACTCTGATGAGCCAGGGACTTACAACTGAGCTAGCTAGCTGGCCT 1421
 Qy 382 ValLeuIhrAlaLeuLeuIhrArgLysIleLeuAspGluIleGluAlaAspSptYr 401
 DB 1422 GTATGGGATCTTGGCTTGTACCGGCAAATACTGGACAGATGTGACATTGAC 1481
 Qy 402 AspAsnPheThrArgArgAlaTyValSerLysProLysLysGlyValThrLeuProfile 421
 DB 1482 AACACTCACAAAGAGCTATGAGCTATTCCTTAATT 1541
 Qy 422 AlaTyraAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
 DB 1542 GCCTATGGAAAATCTCTGTGCCCCCTACAAGAACTCTGTGACCTCTAGCTAAAG 1596
 RESULT 5
 AAU03878

DE	Db	531. -----TCGTAAGGTCGTATGGTGTACACGGCGGAGAAATGGGGACGATG 581
XX	Qy	102 SerGluLysLysValTyrAspValLeuLysGinAlaAlaLeuVallysArgGln 121
KW	Db	582 ACATCAGAACAGATGGTTATGTTAAACAGCAGCTTATGAAAGGGCAG 641
ultra violet absorber; food colour; ss.		
XX	Qy	122 LeuArgSerThrAspAspLeuGlutVallysProAspIleValProGlyAlaLeuGly 141
OS	Db	642 TTGAGATCTGCTGATGATTAGAATGAGCCGGAGATCCCTCCTCCGGAAATTGAGTC 701
Nicotiana tabacum.	Qy	142 LeuIeuSerGluAlaTytaSpaPargCysGlyLysGluVallysAlaLysThrPhe 161
XX	Db	702 TTGTGACTGAAGCATATGATGGTAGTGTAGGTTAGTGCAGGTATGCAAGCATTT 761
FH	Qy	162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPheAlaIleThrVal 181
CDS	Db	762 TACTTAGAACCATGCTATGACTGATGAAAGGGCTATTGGCCAATATATGTC 821
FT	Qy	182 TrpCysArgArgGlyArgGluLeuValaspGlyProAlaLaserHisIleThrProGln 201
FT	Db	822 TGGTGCAGGAGAACAGATGAACTGTGATGGCCAAACGCACTACAGTTACACCCAA 881
/*tag= a.	Qy	202 AlaLeuAspArgTrpGluThrArgLeuGluAspIleSerGlyArgProPheAspMet 221
XX	Db	.882 GCCTAGATAGTGGGAGACCCTGTAAGATGTTTCAGGGCGACCATTTGATGATG 941
XX	Qy	222 LeuAspAlaAlaIeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
XX	Db	942 CTCGATGCTGCTGTTCCAGTTGATATTGCTCAAGCTGTTGATATTGAGCTTCAGA 1001
(DELL/)	Qy	242 AspMetIleGluGlyMetArgMetArgNetaSpLeuItpLyserArgTrpLysThrPheAspGlu 261
DELL/	Db	1002 GATATGATTGAGGAATCGTATGACTGTTGACTGAACTTAAGATAGAACTTGATGAG 1061
DELL/	Qy	262 LeuItyrLeuItyrCystTyryValAlaGlyIleValGlyLeuMetSerValProValMet 281
DELL/	Db	1062 CTTACCTCTATGTTATACGTTGCTGTTGACTGGTTGGTTGATGAGTTGTTCCATTATG 1121
DELL/	Qy	282 GlyIleAlaProGluSerLysAlaThrIhrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
DELL/	Db	1122 GGATTCGACCTGATTCAAAGGCAACACAGAGCGPATATAATGACCTTGTGCTTTA 1181
DELL/	Qy	302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuAlaAspAlaArgGlyLysAlaAspAlaArgGly 321
DELL/	Db	1182 GGATCGGGAAATCAACTAACGAACTACTCAGGATGTTGGAGAAGATGGCCAGAGGAA 1241
DELL/	Qy	322 ArgValIleLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspLysIlePhe 341
DELL/	Db	1242 AGGTCTACTTACCTCAGATGATTACACGAGGTCTCTGCAGCATGAGATATT 1301
DELL/	Qy	342 AlaGlyArgValIhrAspLysTrpArgAsnPhemethylsLysGlnIleGlnArgAlaArg 361
DELL/	Db	1302 GCTGAAAGTGACTGATGATAAGTGAGAAGCAATCCAGGGCAAGA 1331
DELL/	Qy	362 LysPhePheAspGluUserGluLysGlyValThrGluLeuAspSerAlaSerArgTriPpO 381
DELL/	Db	1362 AACTCTGATGAGCCAGGGACTTACAACTGAGCTAGCTAGCTGGCCT 1421
DELL/	Qy	382 ValLeuIhrAlaLeuLeuIhrArgLysIleLeuAspGluIleGluAlaAspSptYr 401
DELL/	Db	1422 GTATGGGATCTTGGCTTGTACCGGCAAATACTGGACAGATGTGACATTGAC 1481
DELL/	Qy	402 AspAsnPheThrArgArgAlaTyValSerLysProLysLysGlyValThrLeuProfile 421
DELL/	Db	1482 AACACTCACAAAGAGCTATGAGCTATTCCTTAATT 1541
DELL/	Qy	422 AlaTyraAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
DELL/	Db	1542 GCCTATGGAAAATCTCTGTGCCCCCTACAAGAACTCTGTGACCTCTAGCTAAAG 1596
DELL/	Qy	RESULT 5
DELL/	Db	AAU03878

ID	AAV03878	standard; cDNA: 1795 BP.
XX	AAV03878;	
AC		
XX	29-APR-1998	(first entry)
DE	Phytoene synthase coding sequence from <i>N. benthamiana</i> .	
XX	Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;	
KW	ultra violet absorber; food colour; ss.	
XX	<i>Nicotiana benthamiana</i> .	
XX	Key	Location/Qualifiers
FH	FT	361..154
CDS	FT	/*tag= a
XX	PN	US5705624 A.
XX	XX	06-JAN-1998.
PD	XX	27-DEC-1995; 95US-0579667.
PF	XX	27-DEC-1995; 95US-0579667.
PR	XX	(DELL/) DELLA-CIOPPA G R. (FITE/) FITZMAURICE W P. (GRILL/) GRILL L K. (HELM/) HELLMANN G M. (KUMA/) KUMAGAI M H.
PA	XX	Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;
PI	XX	DR: 1998-086196/08. DR-PDB: AAW41570.
XX	XX	DNA encoding tobacco phytoene synthase polypeptides - useful for producing recombinant polypeptides or transgenic plants
PT	XX	Claim 1: Column 15-20; 25pp; English.
CC	XX	This sequence encodes the phytoene synthase from <i>Nicotiana benthamiana</i> . The phytoene synthase coding sequence represents a cDNA of the invention. The isolated nucleic acid molecules are used for producing recombinant polypeptides or transgenic plants with enhanced ability to synthesize carotenoids. Phytoene has been used as a ultra violet absorber and other carotenoids have been used as food colours, animal feeds and in the pharmaceutical and cosmetics industries.
CC	XX	Sequence 1795 BP; 577 A; 271 C; 434 G; 513 T; 0 other;
PS	XX	Alignment Scores:
Pred. No.:	1	Length: 1795
Score:	1.75e-180	
Percent. Similarity:	87.07%	Matches: 351
Best Local Similarity:	79.55%	Conservative: 33
Query Match:	78.15%	Mismatches: 28
DB:	19	Indels: 29
		Gaps: 4
US-09-847-0818-2 (1-440) x AAV03878 (1-1795)		
QY	1	MetSerMetSerValAlaLeuLeuIrrPvalValSerProThrSerGluValSerAsnGly 20
DB	356	CTCGAATCTGTGGATTCAATTGGGTTTGAATTCGAGCTAACATGAGCTGAGCT 412
QY	21	ThrgLYLeuLeuaspSerValArgGluGlyAspArgValPheValSerArgPheLeu 40
DB	413	ACAGATCTTGGATTCAATTGGGTTTGAATTCGAGCTAACATGAGCTGAGCT 469
QY	41	AlaArgAspArgAsnLeuMetTrpAsnGlyArgLileLysGlyGlyArgGlnArgTrp 60
DB	470	AGAAATTTGTTGTCGAATGAGGAAACAGAGAGGTTGCAATTGAGGAAACAGAGCTG 520
QY	61	AsnPheGlySerLeuIleAlaAspProArgTyrrSerCysLeuGlyGlySerArgThrGlu 80
DB	521	AATTGGT----- 521
QY	81	LysGlySerThrPheserValGlnSerSerIeuValAlaSerProAlaGlyGluMet--- 99
DB	530	TCTGTAAGGCTGCTGCTATGGTTAGCTACCGGGGGAAATGGCG 574
QY	100	ThrValSerGluLysValtyAspValValLeuLysGlnAlaAlaLeuValLys 119
DB	575	ACGATGACATCACAGACAGGGTTAACACAGCTTATGGAAAG 634
QY	120	ArgGlnLeuArgserThrAspAspLeuGluValyProAspIleValProGlyAsn 139
DB	635	AGGCAGTTGAGATCAGTACTGATGATGATGAGCATATGAGTAGTGGAAAG 694
QY	140	LeuGlyLeuLeuSerGluLataTrpAspCysGlyGluValCysAlaGluTyraAlaLys 159
DB	695	TTGACCTTGTTGAGGAAGCATATGAGTAGTGGAAAGTAGTGGAAAT 754
QY	160	ThrPheTerIeuGlyThrLysLeuMetThrProGluTgAGGAGAlaIleTrpAlaIle 179
DB	755	ACATTTTACTTGGACCACTGCTATGACTCAGGCTATGGGAAATA 814
QY	180	TyrValTrpCysArgArgGthrasPgluLeuValAspGlyProAsnAlaSerHisIleThr 199
DB	815	TATGATGGTCAGGAGAACAGATGACTGTTGATGCCGAAATCATTAC 874
QY	200	ProGlnAlaIeuAspArgTrpGluIthrArgLeuGluAspIlePheSerGlyArgProPhe 219
DB	875	CCACAGGCTTAAAGGTGGAAACCTGCTGTTACTGGGGCCATT 934
QY	220	AspMetLeuAspAlaAlaLeuSerAspThrValSerAspThrValSerGlyPro 239
DB	935	GATANGCTCATGCTGCTTGTGCTGCTTCAAGTTCAGTTGATATTGCGCCA 994
QY	240	PheArgAspMetIleGluGlyMetArgMetAspLeuTrpLyserArgTyrlsThrPhe 259
DB	995	TTCAGAGATATGATGATGAGGAATGGGATATGGACTTAGGGCTAGATAGAACTTT 105
QY	260	AspGluLeuTerItyLettYrCystYrTrpYrValAlaGlyTerItyMeteSerIalPro 279
DB	1055	GATGGCTATACCTATATGTTATACGTGCTGACGGTTGGTGTATGATGTTCTCCA 111
QY	280	ValMetGlyIleAlaProGluSerIlyAlaThrThrGluSerValItyAspAlaAlaLeu 299
DB	1115	ATTAGGGTATTGCAACCTGATTCAAGGCAACAGAGATGATAATAATGCGCTTGT 117
QY	300	AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuIleArgAspVialyGluAspAlaArg 319
DB	1175	GCTTGGGTATAGCAAACTACAACATACTAGAGATGTCGGAGAAATGCGAGA 123
QY	320	ArgGlyArgValtyIleProGlnAspGluIeuAlaGlnAlaGlyIeuSerAspGluAsp 339
DB	1235	AGAGGAAGACTCTACTTACCTCAAGATTAATGACATGCTCTCGACATGAC 129
QY	340	IlePheAlaGlyArgValThrAspIlysPlysPargAsnPhmMetLysysGlnIleGlnArg 359
DB	1295	ATATCGCTGAAAGTACGGGATAATGGAGAAGCTTATGAAAGAGCAATCCAGAGG 135
QY	360	AlaArgLysIpheAspGluSerGluIysClyValThrGluLeuAspSerIalaSerArg 379
DB	1355	GCAAGAAAGTCTTGTGCTGCTTGTATGAGGCAAGACACTGAGCTAGTGTAGA 141
QY	380	TrpProValIeuThrAlaLeuLeuItyArgLsIleLeuAspIleIleGluAlaAsn 399
DB	1415	TGGCTGTATGGCCTTCAGTGTGCTGCTTGTATGAGGCAAGATCTGACAGCT 147
QY	400	AspPtyAsnAsnPhetherPheAspLysProLysLeuLeuThrLeu 419
DB	1475	GACPTAACAAACTACAAGAGCTTAAAGAGCTTAAAGAGCTTAAATGCTTAA 153

Qy 420 ProlineAlaTyraLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
 Db 1535 CCGATTGGTAATGCAAAATCTCUTGCCCCAACAGAACTCTTGTCTCTTAGCTAA 1594

Qy 439 s 439
 Db 1595 G 1595

RESULT 6
 AAV03879 standard; cDNA; 1316 BP.
 XX
 AC AAV03879;
 XX
 DT 29-APR-1998 (first entry)
 XX Phytoene synthase coding sequence from N. benthamiana.
 DE XX
 KW Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;
 KW ultra violet absorber; food colour; ss.
 XX
 OS Nicotiana benthamiana.
 FH Key
 FT CDS
 Qualifiers
 1..1242
 /*tag= a

XX US5705624-A.
 XX 06-JAN-1998.
 XX PF 27-DEC-1995; 95US-0579667.
 XX (DELLI/) DELLA-CIOPPA G R.
 PA (FITSZ/) FITZMAURICE W F.
 PA (GRILL/) GRILL L K.
 PA (HELI/) HELLMANN G M.
 PA (KOMRA/) KUMAGAI M H.
 PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;
 PI Kumagai MH;
 PS DR; 1998-086196/08.
 DR P-PSDB; AAW41058.

XX PT DNA encoding tobacco phytoene synthase polypeptides - useful for
 PT producing recombinant polypeptides or transgenic plants
 XX Claim 1; Column 21-26; 25pp; English.

XX This sequence encodes the phytoene synthetase from Nicotiana benthamiana.
 CC The phytoene synthetase coding sequence represents a DNA of the
 CC invention. The isolated nucleic acid molecules are used for producing
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesize carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.

SQ Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other;

Db 1 ArgCTCTTGCTGTTGTTGTTTCACCT---TGTGAGGTCTCAATGGGACAGGA 57
 2 LeuLeuAspSerValArgGluglyAshArgValPheValSerSerArgPheLeuAlaLys 42
 3 AspGlyAsnLeuMetTrpAsnGlyArgLileysLysGlyArgGlnArgTrpAsnPhe 62
 4 AspGlyAsnLeuMetTrpAsnGlyArgLileysLysGlyArgGlnArgTrpAsnPhe 62
 58 TTCTGATTCAATCCGGAGGAAACCGGGTTTGTGTTGCTG 105
 63 GlySerLeuIleAlaAspProArgTrt-SercysLeuGlyGlySerArgThrGluLysGly 82
 166 GTG-----168

Db 169 -----169
 83 SerThrPheSerValGlnSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
 169 -----169
 Db 170 SerSerGluLysTrsValTrsAspValValLeuLysGlnAlaLysLeuValLysArgGln 121
 220 ACATCAGAACAGATGGTTTATGATGTTGTTATGCTGTTAGTGAAGGGCAG 279
 171 -----171
 Qy 172 LeuArgSerThrAspLeuGluValWysProAspLeuValAspGlyAsnLeuGly 141
 280 TTGAGACTACTGATGATTAGATGAGGTGAGGGCGAGATCCCTGCCGGAAATTGGAGC 339
 173 -----173
 Qy 174 LeuSerGluAlaTyraAspArgCysCysLysGluValCysAlaGluTrpAlaLysThrPhe 161
 340 TrGTGAGTGAAACCATAATGATAGGTGAGGTATGTGCAGATGATGCGAACACATT 399
 175 -----175
 Qy 176 TyrLeuGlyThrLysLeuMetThrProGluLysGargArgGalaLysPheAlaLysVal 181
 400 TACTTAACTATGCTTAATGACTCCAGAGAAGGGCTATTGGCAATATATGTA 459
 177 -----177
 Qy 182 TrpCysArgArgTrhAspGluLeuValAspGlyProAsnAlaSerHisLeuThrProGln 201
 460 TGGTGCAGGAGAACAGAACGAAACTTGTGATGCCGAAATGTCATACATATACTCCACA 519
 178 -----178
 Qy 202 AlaLeuAspArgTrpGluThrArgLysGluAspIlePheSerGlyArgProPheAspNet 221
 520 GCCTTAGATAGGTTGGAGACCCGCTGGAAGATGTTTCAGTGGCGCCATTGACATG 579
 179 -----179
 Qy 222 LeuAspAlaAlaUserAspThrValSerArgPheProValAspIleGlnProPheArg 241
 580 CTCGATGCGTTGCTGCTGATACTGTTCCAGTTCAACTTCAGTTATTCAGCCGTCAGA 639
 180 -----180
 Qy 242 AspMetIleGluLysMetArgMetAspLeuTrpLyserArgTrpLeuAspGlu 261
 640 GATATGATCAGGGAAATCGTGTGACTTGAGGAAGTCAGAACACTTGATGAG 699
 181 -----181
 Qy 262 LeuTrpIleTrpCystTrtyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
 700 CTATACCTATGTTATTAGTGTGCTGATGTTGACATGTTGCTGAGTTGCAATTAG 759
 182 -----182
 Qy 282 GlyIleAlaProIleUserAspThrValSerValAlaLeuAlaLeu 301
 760 GGATTCGACCTGATCATCAAAGGCAACCARAGAGTGATATATGCAAGCTTGCTTGT 819
 183 -----183
 Qy 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuIleGluAspAlaArgArgGly 321
 820 GGTATCGGGAATCAACTAACCAACTTCAGAGATGCGGAAGAGATGCCAGAGGA 879
 184 -----184
 Qy 322 ArgValtryLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
 185 -----185
 Db 880 AGATCTACTTCACTCAAGATGAAATTACACGAGCTTCGACCATGACATAATT 939
 186 -----186
 Qy 342 AlaGlyArgValThrAspLysTrPArgAsnPheMetLysLysGlnIleGlnArgAlaArg 361
 940 ACTGAAAATGTCAGCTTATGAAAGCCTTATGAAAGCCTTATGAAAGCCTTATGAAAGC 999
 187 -----187
 Qy 362 LysPheAspGluUserGluLysGlyValThrGluLeuAspSerAlaSerArgTrpPro 381
 188 -----188

Db 1000 AAGTCTTCAATGAGGAGGTTACAACTGAGCTAGCATGGCCCT 1059
 QY 382 ValLeuThrAlaLeuLeuLeuUtyArgLysIleLeuAspGluIleGluAlaAspTyr 401
 Db 1060 GTATGGCACTTTCGTGTACCGCCAAATACTCGAGAGTCGAACCAATGACTAC 1119
 QY 402 AsnAsnPheThrArgArgAlaTyValSerLysProLysLeuLeuThrLeuProIle 421
 Db 1120 AACAACTTCACAAAGAGGTATTGACCAAATCAAAARGCTTAACTTCTTACCTAT 1179
 QY 422 AlatYzAlaLysSerLeuValProProAsnArgThr 433
 Db 1180 GCTTATGCCAAATCTCTTGCCCCCTAACAAAGACT 1215

RESULT 7

AAQ99323 standard; cDNA; 1591 BP.
 ID AAQ99323;
 AC AAQ99323;
 XX DT 13-APR-1996 (first entry)
 DE Melon phytoene synthase gene.
 XX melon; phytoene synthase; ripening; cDNA library; fruit; MEL5;
 KW melon; phytoene synthase; ripening; cDNA library; fruit; MEL5;
 KW probe; hybridisation; polymerase chain reaction; PCR;
 KW antisense; transgenic plant; crop improvement; carotenoid; vector;
 KW ss.
 XX Cucumis melo.
 XX PN WO9602650-A2.
 XX PD 01-FEB-1996.
 XX PP 06-JUL-1995; 95WO-GB01603.
 XX PR 22-SEP-1994; 94GB-0010081.
 PR 18-JUL-1994; 94GB-001505.
 XX PA (ZENE) ZENECA LTD.
 PI Grierson D, John I, Karvouni Z, Taylor J, Turner A;
 PI Watson C;
 XX DR WPI; 1996-105912/11.
 XX New isolated DNA encoding melon phytoene synthase - used to
 PT transform plants to modify carotenoid content and related
 PT characteristics in plant parts, partic. fruit
 XX
 PS Claim 2: Page 15-16; 22Pp; English.
 XX The sequence encodes melon phytoene-synthase (MEL5 gene), and is
 CC almost full-length. The sequence has been isolated as a cDNA clone
 CC from a ripening-related cDNA library derived from climacteric melon
 CC fruit, using the tomato phytoene-synthase cDNA (TOM5) as a
 CC heterologous probe. The MEL5 gene 5'-end has also been isolated by
 CC polymerase chain reaction and sequenced. The DNA may be used in
 CC sense or antisense constructs to modify gene expression in plants.
 CC The carotenoid content and related characteristics of plant parts
 CC (particularly fruit) may be modified in this way.
 XX Sequence 1591 BP; 507 A; 237 C; 395 G; 452 T; 0 other; ;

us-09-847-081B-2 (1-440) x AAQ99323 (1-1591)
 Qy 1 MetSerMetSerValAlaLeuLeuLeuUtyArgLysIleLeuAspGluAlaSerIleSerGly 20
 Db 258 CTCAGAATGCTGTCCTGCTGTTATGGGTCTCAATGGG 314
 Qy 21 ThrgIleLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
 Db 315 ACAAGTTCTAGGAATCAGTCGGGAGAACCTTTTTGATTCATCC----- 365
 Qy 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysGlyIleGlyArgGlnArgTrp 60
 Db 366 ---AGCACTAGGAATTTGGTGTCCATAGAGAACTAAATAGGGT----- 407
 Qy 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgPheGlu 80
 Db 408 -----GGGAAANGCAACACTAAT 425
 Qy 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGlyLumetThr 100
 Db 426 AATGGACGGAATTTCTGTAACGGCTACTCTGGCTACTCTGGAGAACGGGACG 485
 Qy 101 ValSerSerGluLysLysValtyAspValValLeuLysGlnAlaAlaLeuValIleSArg 120
 Db 486 ATGACATCGAACAGATGCTCTAGATGNGGTTAGTGGCTGGCTGGTGAAGAG 545
 Qy 121 GluLeuArgSerThrAspAspLeuIleValIleValAspGlyAsnLeu 140
 Db 546 CAACTGAGATCTACCAATGAGTTAGAAGTGAAGGGATAACCTATCCTGGGATTG 605
 Qy 141 GlyLeuLeuSerGluAlaTyAspArgCysGlyGluIvaIcysAlaGluTyrAlaLysThr 160
 Db 606 GGCTGTTGATGTGAGCATATGAGTAGTGGAGTAGTGCAGAG 665
 Qy 161 PheTyRLenglyThryLysIleUMethhrProGluAArgArgAlaIleTrPAlaIleTyr 180
 Db 666 TTAACTTAACTGAAACTATGCTAAATGACTCCGGAGAAAGAGGGCTATCTGGCAATATA 725
 Qy 181 ValItpCysAArgA9ThrAspGluIvaIAspGlyProtnAlaSerHisIleThrPro 200
 Db 726 GTATGGTGCAGAACAGATGAACTTGTGATGCCCAAAACGGCTCATATATCCCCG 785
 Qy 201 GlnAlaLeuAspArgTrpGluIleGluAspIlePheSerGlyArgProPheAsp 220
 Db 786 GCACCTGATAGTTGGAAATAAGGTAGAAGTGTCAAGGGGGCCATTGTAC 845
 Qy 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
 Db 846 ATGGATATGATGGAAATGCGATTTGTCGGATCACGTTCCAGTGTATTCAGCCATT 905
 Qy 241 ArgAspMetIleGluGlyMetArgMetAspLeutrpArgLeuGluAspIlePheSerGlyArgProPheAsp 260
 Db 906 AGAGATATGATGGAAATGCGATTTGTCGGATCACGTTCCAGTGTATTCAGCCATT 965
 Qy 261 GluLeutpLeutrpCystyTrtYrValAlaGlyIleLeuMetSerValProVal 280
 Db 966 GAACATACCTTTATGTTGTTGTCGGATCACGTTCCAGTGTATTCAGCCATT 1025
 Qy 281 MetGlyIleAlaProGlnUserLysAlaLysAlaLysAlaLysAlaLysAla 300
 Db 1026 ATGGGATATGCCCTGAATCAAAGCAAAACAGAGCTATAATGTCGTTGGCT 1085
 Qy 301 LeuglyLeuAlaAspGlnLeuThrAspIleLeuArgAspIleLeuAlaGlnAlaGlyLeu 320
 Db 1086 CTGGGATGCGCAATCAATACTAGAGATGTCGAGAAATGCGCAAGAA 1145
 Alignment Scores:
 Pred. No.: 4.36e-178 Length: 1591
 Score: 1751.00 Matches: 344
 Percent Similarity: 86.6% Conservative: 33
 Best Local Similarity: 79.08% Mismatches: 34
 Query Match: 77.14% Indels: 24
 DB: 17 Gaps: 3

present, but produces the same protein on translation. Transgenic plants with enhanced ability to express a selected can be produced by the method. For example, the method can be used to achieve overexpression of a gene specifying an enzyme necessary for carotenoid synthesis in plants (especially phytene synthase), to enhance carotenoid expression, e.g. overexpression of the carotenoid lycopene responsible for the red colouration of developing tomato fruit. Protein expression is enhanced by inserting a gene construct which is altered by maximising the dissimilarity of nucleotide usage whilst maintaining identity of the encoded protein. Known methods of increasing protein production by gene insertion sometimes result in low or no expression (co-suppression), especially when the recombinant and endogenous gene sequences are similar. The method allows enhanced expression whilst avoiding or reducing co-suppression, since sequence similarity between the two genes is sufficiently reduced.

AAV17247	ID	AAV17247	standard; DNA: 1239 BP.
XX	XX	AAV17247;	
AC	XX		
XX	DT	28-MAY-1998	(first entry)
XX	DE	MTOM5,	modified phytoene synthase gene.
XX	XX	MTOM5;	phytoene synthase; chloroplast targeting sequence; enzyme; tomato; protein expression enhancement; transgenic plant; carotenoid synthesis; lycopene; ds.
KW	KW		
KW	OS	Lycopersicon esculentum.	
XX	XX		
PH	Key		Location/Qualifiers
FT	CDS	1..1239	
FT	FT	/*tag= a	
FT	FT	/note= "contains an intron"	
exon	FT	1..960	
FT	FT	/*tag= b	
FT	FT	/number= 1	
intron	FT	951..990	
FT	FT	/*tag= c	
FT	FT	/number= 1	
exon	FT	991..1236	
FT	FT	/*tag= d	
XX	XX		
PN	PN	WO9746690-A1.	
XX	XX		
PD	PD	11-DEC-1997.	
XX	XX		
PF	PF	97WO-GB01414.	
XX	XX		
PR	PR	07-JUN-1996;	
XX	XX	96GB-0011981.	
PA	(ZENE) ZENECA LTD.		
XX	XX		
Bird CR,	Drake CR,	Schuch WW;	
XX	XX		
DR	WP1; 1998-04-2198/04.		
DR	P-PSDB; AAW41374.		
XX	XX		
PT	Enhancing gene expression without or with reduced co-suppression -		
PT	using altered DNA producing different RNA but same protein as		
PT	natural gene, useful especially in plants to allow overexpression of		
PT	a protein		
PS	Claim 9; Page 15-16; 32pp; English.		
XX	XX	This sequence represents the modified phytoene synthase gene MTOM5, which	
CC	CC	is also a chloroplast targeting sequence. This sequence is used in the	
CC	CC	method of the invention for enhancing expression of a protein by an	
CC	CC	organism, comprising inserting into its genome a nucleotide sequence	
CC	CC	which produces different RNA on transcription to that of the gene already	

QY	143	LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhetyr	162
Db	349	TTGAGCAAGCATATGATAGGTGCTGAATGATGGAGTGTCAAAGACGTTAAC	408
QY	163	IeuGlyThrLysLeuMetThrProGluArgArgGalaIleTrpAlaIleTyrValTrp	182
Db	409	TAGGAACTATGCTATGACTCCGAGAGAAGGGTCATCTGGCAATAATATGATGG	468
QY	183	CYSArgArgThrAspGluLeuValAspGlyProAlaSerHisIleThrProGlnAla	202
Db	469	TGCAGAAAGAACGATCATATTACCCGCCAGGCC	528
QY	203	LeuAspArgTrpGluIthrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu	222
Db	529	CTAGTAGTCGGAAATAAGCTAGAGTAGCTAGAGGTTTCATGGCGCATTGACATGCTC	588
QY	223	AspAlaAlaLeuSerAspThrValSerArgPhePheProValAspIleGlnProPheArgAsp	242
Db	589	GATGGGCTTGTGCTGATGAGTTCTAACCTTCAGTTGATATTCAGCTTCAGAGAT	648
QY	243	MetIleGluGlyMetArgMetAspIleUtrpLysSerArgArgTyrLysThrPheAspGluIleu	262
Db	649	ATGATGAAAGGAAATGGTGTGGACTGTGAGAAAATGGATPACAAGAACCTGACGAACTA	708
QY	263	TyrLeuItyrcystytryvalAlaGlyIthrValGlyLeuMetSerValProValMetGly	282
Db	709	TACCTTTATGTTATATGTTGCTGTTACGGTTGGTTGAGTTGAGTTGGCTCAATTGGGT	768
QY	283	IleAlaProGluSerIlysAlaIthrThrGluSerValTyrasnAlaIleAlaLeuGly	302
Db	769	ATGCCCTGTGATCAAGCCACACAGAGGGTATAATGCTCTTGGCTTGTTGGG	828
QY	303	LeuAlaAsnGlnLeuIthrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg	322
Db	829	ATGCCAAATCTCAATTCTCAACATCTCAGATGTTGGAGAGATGCCAGAGAAAGA	888
QY	323	ValtrylLeuProGlnAspGluLeuIalagInAlaGlyLeuSerAspGluAspIleHeAla	342
Db	889	GTCTACTTGCTCAAGATGTTGATGTTGAGATGTTGGAGAGATGCCAGAGAAAGA	948
QY	343	GlyArgValThrAspIlysTrpArgAsnPhiMetIlysGlnIleGlnArgAlaArgLys	362
Db	949	GGAGGGTGGACCATTAATGGATGAACTCTTATGAGAAACAAATATGGCAAGAAAG	1000
QY	363	PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal	382
Db	1009	TTCTTGATGAGGCCAGAAATGGCTGACGAAATTSAGCTCAGCTAGTATATTCCCTGTA	1066
QY	383	LeuThrAlaLeuLeuItytArgGlyIleLeuAspGluIleGluIalaAsnAspTyrAsn	402
Db	1069	TGGGCACTCTGGCTGTTGACCGCAAAATACTAGATGAGATTGAACCAATGACACAAC	1128
QY	403	AsnPheThrArgArgAlaTyrValSerLysProLysIleLeuThrIleProIleAla	422
Db	1129	AACTTACAAAGAGACATATGTCAGCAAAATTCATGTTACCTATTGCA	1188
QY	423	TyrAlaLysSerLeuValProProAsnArgThrSerSer	435
Db	1189	TATGCCAAATCTCTGTGCCCTCCTACAAAAGCTACTGCCCTCT	1227
RESULT 10			
AAQ12495	ID	AAQ12495 standard; CDNA: 1646 BP.	
XX	XX		
XX	DT	18-SEP-1991 (first entry)	
XX	DE	Tomato fruit ripening related gene pTOM5.	
XX	KW	ripening; lycopene; transgenic tomato; ss.	
OS	KW	Lycopersicon esculentum var. Alisa Craig.	

XX	Key	Location/Qualifiers	
FH		201..1436	
FT		/"tag" a	
FT			
XX		WS0109128-A.	
PN			
XX		27-JUN-1991.	
PD			
XX		90M0-GB01924.	
PF			
XX		10-DEC-1990;	
PR		89GB-0028179.	
XX		12-DEC-1989;	
PA	(ICIL) IMPERIAL CHEM IND'S PLC.		
XX			
P1	Bird CR, Grierson D, Schuch W;		
XX			
DR	WPI: 1991-208154/28.		
XX			
PT	DNA construct to modify synthesis of plant carotenoid(s)		
PT	comprises sequence homologous to gene of clone ptOMS preceded by		
PT	plant promoter		
XX			
PS	Disclosure: Fig 1; 35pp; English.		
XX			
CC	Clone ptOMS was derived from a cDNA library isolated from ripe		
CC	total RNA (Slater et al., Plant Molecular Biology 5, 137-147,		
CC	1985). The protein it encodes is estimated to have mol. wt. ca.		
CC	48kD. ptOMS is expressed in ripening fruit. Strongest expression is		
CC	at the full orange stage of ripening; no expression is detected in		
CC	green fruit. See also AAQ12494.		
XX			
SQ	Sequence 1646 BP; 529 A; 249 C; 387 G; 481 T; 0 other;		
XX			
PS	Alignment Scores:		
XX			
Pred. No.:	1.06e-175	Length:	1646
Score:	1729.00	Matches:	345
Percent Similarity:	95.68%	Conservative:	32
Best Local Similarity:	78.41%	Mismatches:	36
Query Match:	76.17%	Indels:	27
DB:	12	Gaps:	4
US-09-847-081B-2 (1-440) x AAQ12495 (1-1646)			
Qy	1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly	20	
Db	195 CTCAGAACTCTGTGCCCTGTTGGTCTCTCTCT--TGTGAGCTCTCAAATGG	251	
Qy	21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu	40	
Db	252 ACAGTTCACTGGATCATGGATCAGTCGGAGGGAAACCGTTTTTGATTCTATCG-----	302	
Qy	41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGlnArgTrp	60	
Db	303 -- AGGCATAGGAAATTGGGTCCAAATGAGGAATAATASAGGT-----	344	
Qy	61 AsnpheGlySerLeuLeAlaAspProArgItyrSerCysLeuGlyGlySerArgThrGlu	80	
Db	345 -----GGTGAAGGCAACTAT-----	362	
Qy	81 LysGlySerThrPheSerValGlnSerSerIeuValAlaSerProAlaGlyGluMetThr	100	
Db	363 AATGACATCGAAGATGATGGCTATGATGTTGTTGAGGAGGCAGCTTGCTGAACGGACG	422	
Qy	101 ValSerSerGluLysValTyrAspLeuGluValIysProAspIleValProGlyAsnLeu	120	
Db	423 ATGACATCGAAGATGATGGCTATGATGTTGTTGAGGAGGCAGCTTGCTGAACGGACG	482	
Qy	121 GluLeuArgSerThrAspAspLeuGluValIysProAspIleValProGlyAsnLeu	140	
Db	483 CAACTGAGATCTACCAATGAGTAGAGTGAAGCCGATATACCTATCCTGGGAATTG	542	
Qy	141 GlyLeuIeuSerGluAlaLeuTyAspArgCysLysIeuValIysValAlaLeuValAspThr	160	

			PN	JP10084966-A.
		XX	XX	07-APR-1998.
		PD	XX	07-APR-1998.
		QY	XX	17-SEP-1996;
	Db	910	PF	96JP-0245107.
	Db	970	XX	17-SEP-1996;
	QY	200	PR	96JP-0245107.
	QY	200	XX	(IWAT-) IWATE KEN.
	Db	970	PA	XX
	QY	220	DR	WPI: 1998-264853/24.
	Db	1030	P-PSDB:	AAW46962.
	QY	240	XX	phytoene synthase gene - useful for breeding plant of variable flower colour
	Db	1090	PS	Claim 2; Pages 7-9; 15pp; Japanese.
	QY	260	XX	The present sequence encodes phytoene synthase 2. It was isolated from a CDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-53. The phytoene synthase gene is useful for breeding plants with variable flower colours.
	Db	1150	CC	Sequence 1921 BP; 633 A; 296 C; 438 G; 554 T; 0 other;
	QY	280	CC	Alignment Scores:
	Db	1210	CC	pred. No.: 4.11e-157
	QY	300	CC	Score: 1557.00
	Db	1270	CC	Percent Similarity: 81.82%
	QY	320	CC	Best Local Similarity: 71.10%
	Db	1330	CC	Query Match: 68.59%
	QY	340	DB:	DB: 2
	Db	1390	DB:	Gaps: 2
	QY	360	QY	US-09-847-081B-2 (1-440) x AAV16949 (1-1921)
	Db	1450	Db	1 MetSerMetSerValAlaLeuLeuTryptalValSerProThrSerGluValSerAsnGly 20
	QY	380	Db	406 GTTAACATGGTCATTGTTACGTATGGCTGAGTCAGTTGGCTGTGAGTTTGAGTGC 465
	Db	1510	QY	21 ThrglyLeuLeuAspSerValArgLuglyAsnArgValPheValSerArgPheLeu 40
	QY	399	Db	466 AATGTTTCTGGAGCCATTGAGAAAGT 501
	Db	1570	QY	41 AlaArgLuglyAsnGlnLeuMetIpraspLysIgylIgylArgGlnIarg 60
	QY	419	Db	502 TTTCGGATAAAGGTTAACATGGAGAGTTAGAACAGTAGACCCAAGGCT 561
	Db	1630	QY	61 AsnPheGlySerLeuIleAlaAspProArgTyrsSerCysLeu----GlyGlySerArg 78
	RESULT	AAV16949	Db	562 AGATCAGTTATGGGTGGAGATTAGTTATTGCTGAGTAGACTCTGATTAG 621
	ID	AAV16949 standard; cDNA to mRNA; 1921 BP.	QY	79 ThrglyLysGlySerThrPheserValGlnSerSerLeuValAlaSerProAlaGlyGlu 98
	XX	AAV16949;	Db	622 ACCCGGGAAAGAAAGATTATCGGATATCCCAGATAATACTACCCCCGCCAGGAGA 681
	AC		QY	99 MetThrValSerGluLysValSvaltyraspValValLeuysGlnAlaAlaLeuVal 118
	XX		Db	682 ATGACGTGACATGCAAGCTTAAAGCTTGTGCTGTTAAAGCAAGCAGTTGATT 741
	DT	06-JUL-1998 (first entry)	QY	119 LysArgGlnLeuArgSerThrAspAspLeuGluVallysProAspIleValIProGly 138
	XX		Db	742 ATAGACAGTTAGGTGAGTCAGACAAAGCTTATGATGTCGTTAAAGCAAGCAGTTGATT 801
	DE	Nucleic acid encoding phytoene synthase 2.	QY	139 AsnLeuGlyLeuLeuSerGluAlaTyraspArgCysGlyGluValCysAlaGluTyrala 158
	KW	Phytoene synthase; breeding; variable flower colour; ds.	Db	802 AACCGCAACGTGTTGAAGCTATGCTGTGAACTATGTGCTGAATATGCC 861
	XX	Gentiana lutea.	QY	159 LysThrPheIleGlyThrylLeuLeuSerGluArgArgAlaIleTrpAla 178
	PH	Location/Qualifiers	Db	862 AAGTCATTCCTACTGGGAACAGCTCATGACACGGAGAGGGCTTNGCTATGGGG 921
	FT	412..1689	QY	179 IleTerTerValTerPheIleGlySerGlyTerAspGluLeuValAspGlyProAsnAlaSerHistile 198
	FT	/*tag- a	XX	

Db	922	ATATGTGATGGTAGGAGCACATGACCTTGATGGCTAAACCGGTCAAACATA	981
Qy	199	ThrProGlnAlaLeuAsparGtpProluthrArgLeuGluAspIlePheserGlyArgPro	218
Db	982	AATCCAAACGCCGTTGAGATGGTGGAAAGGAAAGATAGAATGTTCAAGGGCRAACT	1041
Qy	219	PheAspMetLeuAspAlaAlaLeuSerAsPThrValSerArgPheProValAspIleGln	238
Db	1042	TTCGATGCTGATGCTGTTATCTGATACCATTAACAGTACCTGAGACATCCAG	1101
Qy	239	ProPheArgAspArgMetAspIleGluGlyMetArgMetAspIleTrpIleSerArgTytIysThr	258
Db	1102	CCATTAGAGATACTATAGAGGATGCGGATGGATCTGAAGAAATCGAGATACTAGAAAT	1161
Qy	259	PheAspGluLeutYIleutYIleutYIleutYIleutYIleutYIleutYIleutYIleutYIleutYI	278
Db	1162	TTCGTTGAGGTGATCTTACTGCTATTAGTGCCTGACAGTTGGCTGATGTTGTCGTA	1221
Qy	279	ProValMetGlyIleAlaProGluIleIysAlaThrThrGluSerValtyrasDalaAla	298
Db	1222	CCATGATGGCATTTGCACCTGAACTGAAAGCACAACAGAAAGTGTGATAATGCGCT	1281
Qy	299	LeuAlaLenglyIleuAlaLenglyIleuAlaLenglyIleuAlaLenglyIleuAlaLenglyI	318
Db	1282	TTATTTGGGATGCGAACCGTGACTAACATCTAGGGATGTTGAGAGATGCGCA	1341
Qy	319	ArgGglyGlyArgValTyRLeuProGlnAspGluLeutAlaGlnAlaGlyLeuSerAspGlu	338
Db	1342	AGAAAGGGAGAGAGTTACCTACCCTTGTGAAAGTACAGACAAATGGGAGATTTTAAAGAGCAAA	1401
Qy	339	AspIlePheAlaGlyArgValThrAspIlePheAspIleGlyAsnPhemetylLysGlnIleGln	358
Db	1402	GACATTTTGCTGGAAAGTACAGACAAATGGGAGATTTTAAAGAGCAAA	1461
Qy	359	ArgAlaArgLysPhePheAspGluSerGlyIysGlyValThrGluLeutAspSerAlaSer	378
Db	1462	AGGGCTAGAAATTCTATGATGANCAGAAAAGCTCCCGGAACTCAAGCTCCCGAGC	1521
Qy	379	ArgGtpProValLeuThrAlaLeuLeuLeutYrArgLysIleLeuAspGluIleuAla	398
Db	1522	AGATGGCTGTTGTTGTTGTTTATGAAATATGTTGATGTTGATGTTGATGTTGATGAA	1581
Qy	399	AsnAspTyrAsnAspPheThrArgArgAlaTyryValSerIysProLysLeuLeuthr	418
Db	1582	ATATGCTACACAATTCACAAATGGCTTAATGAAACAGGAAAGAGCTATTAGCT	1641
Qy	419	LeuProIleAlaTyryAlaIysSerIeu	427
Db	1642	ATGGCTGTACCATGTCAGTCAGTC	1668
RESULT 13			
ID	AAC44162	standard; DNA: 1566 BP.	
XX			
AC	AAC44162;		
XX			
DT	18-OCT-2000	(first entry)	
XX			
DE	Arabidopsis thaliana DNA fragment	SEQ ID NO: 56495.	
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
KW	metabolic pathway; promoter; signal transduction sequence; ss.		
XX			
Arabidopsis	thaliana.		
OS			
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PP	25-FEB-2000; 2000EP-0301439.		
XX			

PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144055.
PR	17-JUL-1999;	99US-0144066.
PR	18-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	20-JUL-1999;	99US-0144332.
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PR	24-JUL-1999;	99US-0144336.
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PR	24-AUG-1999;	99US-0149930.
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PR	29-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	02-SEP-1999;	99US-0152363.
PR	03-SEP-1999;	99US-0153070.
PR	04-SEP-1999;	99US-0155486.
PR	05-SEP-1999;	99US-0155659.
PR	06-SEP-1999;	99US-0154039.
PR	07-SEP-1999;	99US-0154779.
PR	08-SEP-1999;	99US-0155139.
PR	09-SEP-1999;	99US-0155486.
PR	10-SEP-1999;	99US-0155659.

PR	04-OCT-1999;	99US-0157117.
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PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158367.
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PR	22-OCT-1999;	99US-0160910.
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PR	29-OCT-1999;	99US-0162142.
Alignment Scores:		
pred. No.:	1.25E-155	
Score:	1542.00	
Percent Similarity:	81.86%	
Best Local Similarity:	72.11%	
Query Match:	67.93%	
DB:	21	
US-09-847-081B-2 (1-440) x AAC481		
Qy	1 MetSerMetSerValAlaLeuLe	
Db	153 ATGCTTCCTCTGTAGCTT	
Qy	19 AsnGlyThrGlyLeuLeuAsSe	
Db	213 AACAAATGTGGGTGTSTA-----	
Qy	39 PheLeuAlaArgAspArgAsnLe	
Db	252 CTGTTCTCCTGTAG-----	
Qy	58 nArgTrpAsnPheGlySerLeuI	
Db	300 CAGATAACCAACTTGAGTCITC	
Qy	78 gThrGluLysGlySerThrPhes	
Db	339 AGTAGAGAAATT-GGTTGTT---	
Qy	98 uMetThrValSerGluLysL	
Db	392 GATAGCTCTTCATCGAAGAGA	
Qy	118 LysArgGlnLeuArgSerThrA	
Db	452 GAAACAACGCTAAGGCCTCTCTT	

Qy	135	IvalProGlyAsnLeuGlyLeuLeuUserLvalAlaTyrAspArgCysGlyGluValCysAl	155	KW Hybridisation assay; genetic mapping; gene expression control;
Db	512	TCTTCCTGGAGTTGAGTTGATGTTGGCTGAAGCTTAGATGATGGCGAAGTTGCGC	571	KW Protein identification; signal transduction pathway;
Qy	155	agluturyralalaLysThrPheTerTyrIleGlyThrLysLeuMetThrProGluArgArgAl	175	KW metabolic pathway; promoter; termination sequence; ss.
Db	572	TGATATGCTAAAGCTGTATCTGGACGTTCTCTTATGACACCAGAAAGGCCAAATGCC	631	XX Arabidopsis thaliana.
Qy	175	algleTPAlaIleTerTyrValTrpCysArgGlnAspGluLeuValAspGlyProAsnAl	195	XX OS
Db	632	GATTGGCAATCTAACGTTGCGTGTAGAGAAACTGATGAACTGTGAACTTGATGAACT	691	XX PN EP1033405-A2.
Qy	195	aseHisIleThrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspPhePhe	215	XX PR 06-SEP-2000.
Db	692	TTCACATATAACCTCCATGGCTTAAGATAGATGAGAAAGGAAAGGCCAAATGCC	751	XX PR 25-FEB-2000; 2000EP-0301439.
Qy	215	rGlyArgProPheAspMetLeuAspAlaAlaLeuUserAspThrValSerArgPheProva	235	XX PR 25-FEB-1999; 99US-0121825.
Db	752	TGGTGTGTCCTTCGATATGCTTGATACAGTGGCTGATACAGTGGCTGATACAGTGG	811	XX PR 09-MAR-1999; 99US-0123180.
Qy	235	LaspIleGlnProPheAlaGlyAspMetIleGluGlyMetAlaLeuTrpLysserAr	255	XX PR 23-MAR-1999; 99US-0123548.
Db	812	CGATATTGCCTCATTCGAGACATGATGAAAGATGAGAAATGCTGAGATCAG	871	XX PR 23-MAR-1999; 99US-0125788.
Qy	255	gTfIleTyrThrPheAspPheGluLeuTerTyrLeuThrCystYrrTyrrValAlaGly	275	XX PR 25-MAR-1999; 99US-0126264.
Db	872	ATACAGAACATTCTGATGCACTATACCTTACTGCTACTAGTGTGAACTGGCTGGATT	931	XX PR 01-APR-1999; 99US-0126785.
Qy	275	uMetSerValProValMetGlyIleAlaProGluSerLysAlaThrGluSerValty	295	XX PR 01-APR-1999; 99US-0127462.
Db	932	GATGAGCGTTCGGTATGGAAATCGATCTAACCTGAAACCGAAAGCTGTTAA	991	XX PR 06-APR-1999; 99US-0128234.
Qy	295	rashAlaAlaLeuAlaLenglyLeuAlaAsnGlnLeuThrAsnIleHargAspVyalG	315	XX PR 08-APR-1999; 99US-0128714.
Db	992	CAACCTGCTGCTTGGCCCTTGGTATGCCATTACGCTACTAACATACTGAGACGTAG	1051	XX PR 16-APR-1999; 99US-0129845.
Qy	315	YGiuaSpLaAarArgGlyArgValAlaTerPheAspGluLeuAlaGlyLe	335	XX PR 19-APR-1999; 99US-0130077.
Db	1052	CGAGATGCGCAGAGAGGGTTATCGCTCAGGGTGAATGGCTCAGGTTCT	1111	XX PR 21-APR-1999; 99US-0130449.
Qy	335	uSerAspGluAspPheAlaGlyArgValAlaTerPheAspLsTrpArgAsnPhMe	355	XX PR 23-APR-1999; 99US-0130510.
Db	1112	TTCAGATGAGACATATTCCCGGAAACTAACTGATAATGGAGAAACTCTGATAAAAT	1171	XX PR 23-APR-1999; 99US-0130891.
Qy	355	sGlnIleGlnArgAlaArgLysPhePheAspGluLysGlyValThrGluLeuAs	375	XX PR 28-APR-1999; 99US-0131449.
Db	1172	GCAGCTTAAACGCAAGAATGCTCTTCGAGAAAGCTGANGAAAGCTGANGAA	1231	XX PR 30-APR-1999; 99US-0132048.
Qy	375	pSerAlaSerArgTrpProValLeuThralaLeuLeuTerLysLeuAspG1	395	XX PR 30-APR-1999; 99US-0132407.
Db	1232	TGCCCTAGAGATGGCTCATGGCTATGCTATGAGAACTGAGAACTGAGCA	1291	XX PR 04-MAY-1999; 99US-0132484.
Qy	395	uIleGluAlaAsnAspPheAsnAsnAspPheAsnAsnAspPheAsnAspPhe	415	XX PR 05-MAY-1999; 99US-0132485.
Db	1292	GATTGAGCGAAATGATTACACATTACTAGAGCTATGGGGAAAGTCAGAA	1351	XX PR 06-MAY-1999; 99US-0132486.
Qy	415	sLeuLeuThrLeuProIleAlaTerAlaTerAlaTerAlaTerAlaTerAlaTer	435	XX PR 07-MAY-1999; 99US-0132487.
Db	1352	AATTGCGCTTGGCATTGGCTATGCTAAATCAGTACTA-----AGACTTCAAG	1402	XX PR 11-MAY-1999; 99US-0132863.
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Db	1403	T 1403		XX PR 14-MAY-1999; 99US-0134219.
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AC				XX PR 14-MAY-1999; 99US-0134221.
XX				XX PR 14-MAY-1999; 99US-0134221.
DE				XX PR 14-MAY-1999; 99US-0134221.
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PR				XX PR 14-MAY-1999; 99US-0134221.
21-JUN-1999				XX PR 14-MAY-1999; 99US-0134221.
22-JUN-1999				XX PR 14-MAY-1999; 99US-0134221.

PR 23-JUN-1999; 990S-0140353.
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 PR 19-JUL-1999; 990S-0144332.
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 PR 25-AUG-1999; 990S-0150566.
 PR 26-AUG-1999; 990S-0150884.
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 PR 30-AUG-1999; 990S-0151303.

PR 31-AUG-1999; 990S-0151438.
 PR 01-SEP-1999; 990S-0151930.
 PR 07-SEP-1999; 990S-0152363.
 PR 10-SEP-1999; 990S-0153070.
 PR 13-SEP-1999; 990S-0153758.
 PR 15-SEP-1999; 990S-0154018.
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 PR 20-SEP-1999; 990S-0154779.
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 PR 29-OCT-1999; 990S-0162142.

Alignment Scores:
 Pred. No.: 1.41e-155
 Score: 1542.00
 Percent Similarity: 79.29%
 Best Local Similarity: 70.98%
 Query Match: 67.93%
 DB: 21
 Gaps: 8

Length: 1703

Qy 1 MetSerMetSerValAlaLeuLeutrpValVai-----SerProThrSerGluValSerArg
 Db 290 ATGTCTTCCTGAGTGTATGGTTGCTACTCTCTAAATCAGACCCAAATG 349

Qy 19 AsnGlyThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArg
 Db 350 AACATTCCTGGTTGGTA-----AGGTCTAGAATCTCTAGA 388

Qy 39 PheLeuAlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysGlyGlyArgGln 58
 Db 389 CIGTCCTCCCTGTCGAAT-----CAG 412

Qy 59 ArgTrpAsnPheGlySerIleLeuAlaAspProArgTyrSerCysLeuGlyGlySerArg
 Db 413 AGCTAACAAAGCTAACAGAACAGATAACCAACTGGAT-----

Qy	79	ThrGlutLySerThrPhe-----	SerValGlnSer	89		Qy	427	LeuValProProAsnArgThrSerSer	435
Db	455	-----TCCTCTTGTAAATGAACCGAAGTAGAGAAATGGTGTGTTCA	502			Db	1523	GTTACTA-----AGACTTCAGT	1540
Qy	90	serleuvalalaserproAlaglyGluLysThrValSerSerGluLysValTyRasp	109			RESULT 15			
Db	503	AGCTTAGTAGCAAGTCCTCTGAGAGATAAGCTCTCATCTGAGAAAGTTCAAT	562			AAV16948			
Qy	110	ValValleuLysGlnAlaAlaLeuValLysArgGlnLeuArgSerThrAsp--AspLeu	128			ID AAV16948 standard; cDNA to mRNA;	2085	BP.	
Db	563	GGTGTTGAAACAAAGCTGGTCAACACAGCTAACGTTCTCTATGATCT	622			XX			
Qy	129	GlutValLys----ProAspIleValIleProGlyAsnLeuGlyLeuLeuSerGluAla	146			DE	Nucleic acid encoding phytene synthase 1.		
Db	623	GATGTGAAAACCACAAAGATCTGTCCTGGGAGTTGAGTTGTTGGTGAAGCT	682			XX	Phytene synthase; breeding; variable flower colour; ds.		
Qy	147	TyrAspPArgCysGlyGluValCysAlaGluTyralaLysThrPheTyrlLeuLys	166			XX	Gentiana.lutea.		
Db	683	TATGATCGATGCGGTGAAGTTGCGCTGAATGCTGAGCTTATCTGGAACTTGT	742			OS			
Qy	167	LeuMetThrProGluArgArgAlaIleThrPAlaIleTyryaIrrPcysArgArgThr	186			Key	Location/Qualifiers		
Db	743	CTPATGACACCCAAAGCGAAAGGCCATTGGCCTACGTTGTTGTTGAGAAAGACT	802			CDS	586..1866		
Qy	187	AspGluIleValAspGlyPyrrolylAlaSerHisIleThrProGlnAlaLeuAspArgTrp	206			FT	/*tag= a		
Db	803	GATGAACTTGTGATGGCCCAAATGCTCACATATACTCCCATGGTTAGATAATGG	862			FT			
Qy	207	GlutThrArgLeuGluAspIlePheSerGlyIaArgProPheAspMetLeuAspAlaLeu	226			PN			
Db	863	GAAGCCAAGTTGAAAGATCTTTCGCGNTGCTGCTCTTCGATATGCTGTAATGCTCTC	922			XX			
Qy	227	SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly	246			PD	07-APR-1998.		
Db	923	GCTGATACTAGTCCTAGATACCTCTGATATTTCAGCCATTGAGCATGATGAGA	982			XX			
Qy	247	MetArgMetAspIleutPheLysSerArgTyrlsThrPheAspGluIleutTyrlutuTyrcys	266			XX			
Db	983	ATGAAATGACTGAAATCGAGATACCAACTCGATGATCTATACCTTTATGC	1042			PS	Claim 1; Pages 5-7; 15pp; Japanese.		
Qy	267	TyrrTyrylValAlaGlyIleValGlyLeuMetSerValProValMetGlyIleAlaProGlu	286			XX			
Db	1043	TACTACGTCGCTGCGAACCGTCGSGATTGATGACGGTTCCGGTATGGGAATTCCTAAAG	1102			CC	The present sequence encodes phytoene synthase 1. It was isolated from a cDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-33. The phytoene synthase gene is useful for breeding plants with variable flower colours.		
Qy	287	SerLysAlaThrThrGluUserValtyrasAlaAlaLeuAlaLeuAlaLeuAlaAsnGln	306			XX	Sequence 2085 BP; 654 A; 320 C; 479 G; 632 T; 0 other;		
Db	1103	TCGAAGACACACCGAAAATGGTTACACGGTTGGCTTGCCCTTGTTAGCCAAATCAG	1162			SQ			
Qy	307	LeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgLysValTyrlLeuPro	326			Alignment Scores:			
Db	1163	CTTACTAACTACTCAGAGCTAACTTCGAGCTAAAGGCAAGAATGCTCTTCGAGAA	1342			Pred. No.:	2.89e-154		
Qy	327	GlnAspGluIleAlaGlnAlaGlyLeuUserAspGluAspIlePheAlaGlyArgValThr	346			Score:	1551.00	Length:	2085
Db	1223	CAGGATGATTGCTCAGTCAGTCAGTGAACGATAATTCGCGGAAAGTAAC	1282			Percent Similarity:	82.56%	Matches:	310
Qy	347	AspIystPArgasnPheMetLysLysGlnIleGlnArgAlaArgLyspheAspGlu	366			Best Local Similarity:	72.09%	Conservative:	45
Db	1283	GATAATGGAGAAACTCTGAGCTAAAGGCAAGAATGCTCTTCGAGCAAA	1342			Query Match:	67.44%	Mismatches:	64
Qy	367	SerGluLysGlyIvaLthgIleLeuAspSerAlaSerArgTrpValLeuThrAlaLeu	386			DB:	19	Indels:	12
Db	1343	GCAGAGAAAGGGTCAAGGAGCTAGGGAGCTAGGGCTAGCATGGCTCATGGCTCATGG	1402			Gaps:	3		
Qy	387	LeuLeutTyrylValGlyIleLeuAspLysLeuLeutThrLeuProLeuAlaAsnAspTyraAsnAspPheThrArg	406			US-09-847-081B-2 (1-440) x AAV16948 (1-2085)			
Db	1403	CTATGTCAGGAGAAATGCTGAGATGAGATGATTACAATTTACTAAG	1462			Qy	1	MetSerMetSerValAlaLeuLeutIleValValSerProThrSerGluValSerAsnGly	20
Qy	407	ArgAlaTyrylValSerLysProIysLysLeuLeutThrLeuProLeuAlaAsnAspPheThrArg	426			Db	580	GTTAACATGTCATTGTTACGTTGATGTTGAGTTGAGTTGAGTC	639
Db	1463	AGACCTTATGTGGGAAAGTCAGGAAATGGCTTGTGCCCCATGTTATGCTAAATCA	1522			Qy	41	AlaArgAspArgAsnLeuMetIleTrpAsnDlyArgIleLysGlyGlyArgGinArgTrp	60
Qy	41	AsnPheGlySerIleLeuAlaAspPheThrLeuProLeuAlaAsnAspPheThrArg	60			Db	676	TTTCGATGATGAACTGTTGACATGTTGAGTACGTTGAGTCACCAAGGGGT	735
Db	736	AGTACACGTTATGGGTTGGAGATTGAGACTTCATTTCGTTGAGATCTGATATAG	795			Qy	61	AsnPheGlySerIleLeuAlaAspPheThrLeuProLeuAlaAsnAspPheThrArg	80

81 ---LysGlySerThrPheSer-ValGlnSerSerLeuAlAlaserProAlaGlyGluMe 99
 Qy :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 796 ACCCGGGAGAAGATTACGGPATCCGCCATATTAGCTAACCCCGCAGGAAAT 855

99 tThrValSerSerGluLysLysValTyrosPvalValLeuLysGlnAlaAlaLeuValY 119
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 856 GACATG-ACATCAGGCAAAAGTTATGCTGGTTAAAGCAAGCCTTGATTA 914

119 sArgGlnLeuIargSarIaAspAspLeuGluValIysProAspIleValProGlyAs 139
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 915 TAGCAGTCTAGGCTAGAGAAATTGGAGTAAACCGACATTATTGCGAGGA 974

139 nLeuGlyLeuLeuSerGluAlaItyrAspArgCysGlyLuIcysAlaGluItyrAlaI 159
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 975 CGCGACGCTTGATGAGCTTATGATGGTGTGAGAGTATGCTGAATGCCNA 1034

159 sThrPheItyrLeuGlyThrLysLeuMetIhrProGluIaGargArgAlaIleItpPala - 178
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 1035 GTCACTCTACTGGGAAACCCAGCTCATGCACCGGAGGGCCTTAGCTATCGGCCGA 1094

Qy 179 -IleItyrValTrpCysArgArgGthrasPleIleValAspGlyProAslAlaSerHisI 198
 Db 1095 TATATATGATGGCTAGGAGACAGATGAGCTGTGTGTGGCTAACCGTCACACAT 1154

198 eThrProGlnAlaIleuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyAtgPr 218
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 1155 AAATCCACCGCGCTTAGATGGTGGAAACCAAGATCAGAGATTTTCACAGGGCAAC 1214

218 oPheAspMetLeuAspAlaAlaLeuAspThrValSerAspHpheProAlaSpIleI 238
 Qy :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
 Db 1215 TCTGGATAATCTGTATGCGCTTATCIGATACTTACCAAGTATCTGTGACATCCA 1274

Qy 238 nProtheArgAspMetIleGluGlyMetArgMetAspIleTrpLysSerArgTrpLysTh 258
 Db 1275 GCCATTAGGATATGATGAAGGAAATGGGATGATCGAAGAAATCCAGATAACAAGA 1334

Qy 258 rPheAspGluLeuItyrLeutyrCystyTrpItyrValAlaGlyItyrValGlyLeuMetSerVa 278
 Db 1335 TTTCATGACTGATCTTACTGTCTATGCTGCTGCACACTTGGCTTGATGAGCT 1394

Qy 278 lProValMetGlyIleAlaProGluSerIysAlaIthrThrGluSerValtyrAsnAlaI 298
 Db 1395 ACCACTAATGGCATTGCAACCTGAACTCPAAGGAAACACAGAAAGTCATATGTCAGC 1454

Qy 298 aLeuAlaIaGlyLeuAlaAsnGinLeuIhrAsnIleuAspGlyItyrValGlyIaAspAl 318
 Db 1455 TTTCATCTTGGGATGCGCAACAGCTGCTAATCTAACTCTAAGGTATGTTGAGAGATGC 1514

Qy 318 aArgArgGlyIargValItyrLeuProGlnAspGluIleuAlaIaGlyIleuSerAspC1 338
 Db 1515 AAGAAGGAGAGGTACCTACCTCAACATGATTACAGCAACCAACGCTTATCAGATGA 1574

Qy 338 uAspIlePheAlaGlyIargValIaAspIstPargAspHpheMetIysGlnIleG 358
 Db 1575 GGACATTTTGCTGCTGAAAGTTACAGAACATGGAGGATTTTATGAAAAGCAANTCA 1634

Qy 358 nArgAlaArgLysPheAspGluSerIleuIysGlyIvalIhrGluLeuAspSerAlaSe 378
 Db 1635 AAGGGCTAGAAARTCTATGATGATGAGAAGGAGCCGAACTACAGCCTCGCGCAG 1694

Qy 378 rArgTrpProValLeuIhrAlaIleuIleuItyrArglysIleuAspGluIleGluAl 398
 Db 1695 CAGATTGCTGTGCTGGCGAGCTGCTTATGAGAAATATTGGATGAGTAGAGC 1754

Qy 398 aAspAspItyrAsnIinPheIhrArgGlnAlaItyrValSerLyProIysLeuLeuIth 418
 Db 1755 AAATGACTCAACAAATTGCGCCAGAGGCTTATGTAACAGGGCGAAGAGCTTATGC 1814

Qy 418 rLeuProIleAlaItyrAlaIlysserLeu 427
 Db 1815 TATGCCCTGPIAGCATGTGCCAAAGTCCTC 1842